FAIR Principles and the Immune Epitope Database

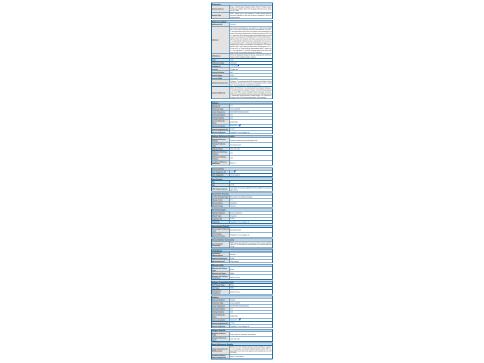
James A. Overton; Knocean Inc. Randi Vita, Alessandro Sette, Bjoern Peters; La Jolla Institute Christopher J. Mungall; Lawrence Berkeley National Laboratory The Immune Epitope Database

The IEDB by the Numbers

A publicly available database of experiments demonstrating recognition of immune epitopes by adaptive immune receptors.

- established 2004 by NIAID
- based at the La Jolla Institute of Allergy and Immunology
- ▶ 18,804 journal articles + direct submissions
- ▶ 1,509,095 assays (individual experiments)
- ▶ up to 400 fields per assay
- ▶ 385,446 epitopes

Epitope		
Epitope ID	717	
Chemical Type	Linear peptide	
Linear Sequence	ADLMGYIPLVGAPLGGAARA	
Starting Position	131	
Ending Position	150	
Source Molecule Name	polyprotein	
Source Accession	BAA03375.1 🗗	
Source Organism ID	31647	
Source Organism	Hepatitis C virus subtype 1b	







To be Findable:

- ▶ F1. (meta)data are assigned a globally unique and persistent identifier
- ▶ F2. data are described with rich metadata (defined by R1 below)
- ► F3. metadata clearly and explicitly include the identifier of the data it describes
- ▶ F4. (meta)data are registered or indexed in a searchable resource

To be Accessible:

- ▶ A1. (meta)data are retrievable by their identifier using a standardized communications protocol
 - ▶ A1.1 the protocol is open, free, and universally implementable
 - ► A1.2 the protocol allows for an authentication and authorization procedure, where necessary
- ▶ A2. metadata are accessible, even when the data are no longer available

To be Interoperable:

- ▶ I1. (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.
- ▶ 12. (meta)data use vocabularies that follow FAIR principles
- ▶ 13. (meta)data include qualified references to other (meta)data

To be Reusable:

- ▶ R1. meta(data) are richly described with a plurality of accurate and relevant attributes
 - R1.1. (meta)data are released with a clear and accessible data usage license
 - ▶ R1.2. (meta)data are associated with detailed provenance
 - ▶ R1.3. (meta)data meet domain-relevant community standards

Summary: FAIR and Square

F1	Persistent IDs	
F2	Rich Metadata	
F3	Metadata Links to Data	
F4	Metadata Indexed	
A1	Open Protocols	
A2	Metadata Remain Accessible	
l1	Open Language	
12	Open Vocabularies	
13	Metadata Links to Metadata	
R1	Rich Metadata	
R1.1	License	
R1.2	Provenance	
R1.3	Community	

Discussion: A FAIR Shake



The distinction between data and metadata is not always clear or helpful.

For the current purposes, the IEDB is a repository of metadata.

Principles and Practises

FAIR principles tell us **what** to do, and sometimes **why** to do it.

They do not tell us **how** to do it.

Shared principles are not enough for interoperability.

FAIR and OBO

The Open Biomedical Ontologies (OBO) community has a set of principles, much in the same spirit as FAIR.

More importantly, OBO also has shared best practises, common infrastructure, open source tooling.

We see an important role for OBO to articulate shared best practises that make the FAIR principles concrete and effective.

My Opinions

	Principle	Practise
F1	Persistent IDs	IRIs and a PURL system
F2	Rich Metadata	RDF(S), OWL, DC, PROV, OBO metadata
A1	Open Protocols	HTTP(S), RDF/OWL in XML, JSON-LD
I 1	Language	RDF/OWL
12	Vocabularies	OBO community
R1.1	License	Creative Commons: CC-BY or CC0
R1.2	Provenance	PROV
R1.3	Community	OBO community

The IEDB: FAIRly Good

F1. Persistent IDs

The IEDB has persistent URLs for assay, reference, epitope:

- http://www.iedb.org/assay/1288922
- http://www.iedb.org/reference/1001817
- http://www.iedb.org/epitope/717

F2. Rich Metadata

Providing rich metadata about experiments is the heart of the IEDB mission.

We can do better!

- use standardized predicates
- share richer modelling
- ► RDF/OWL representation

F3. Metadata Links to Data

The IEDB links to journal articles by PubMed ID.

We also capture more specific location within the document (as free text): figure X, table Y.

We can do better!

- standardized, formalized location data
- link out to PubMed Central structured representations

F4. Metadata Indexed

The IEDB is itself an indexed, searchable resource.

We have also submitted our data to:

- Biosharing
- bioCADDIE
- ► Wikidata

A1. Open Protocols

The IEDB is:

- accessible by HTTP, no authentication required
- published as HTML pages and CSV tables

We can do better!

- CSV with IRIs and labels
- ▶ RDF/OWL representation as JSON-LD or RDFa

Google Structured Data Testing Tool





NEW TEST





Unspecified Type

All (1) ▼

Unspecified Type 0 ERRORS 0 WARNINGS

@type Unspecified Type

https://creativecommons.org http://purl.org/dc/terms/license /licenses/bv/4.0/

https://scicrunch.org/browse http://www.w3.org/ns/prov#wasGeneratedBy /resources/SCR_006604

A2. Metadata Remain Accessible

Published journal articles remain accessible, even if retracted.

The IEDB metadata records will remain accessible in any case.

I1. Knowledge Representation Language

The IEDB uses SQL and publishes in HTML and CSV.

We can do better!

- CSV exports with IRIs and labels
- ▶ RDF/OWL representation in JSON-LD or RDFa

12. FAIR Vocabularies: Reuse

The IEDB links to a wide range of resources:

- UniProt
- GenBank
- ► NCBI Taxonomy
- ► PDB
- ► IMGT
- ► many OBO ontologies
- more...

12. FAIR Vocabularies: Contributions

The IEDB contributes whenever possible:

- ► Ontology for Biomedical Investigations (>300 terms)
- ► Disease Ontology (>200 terms)
- ► Chemical Entities of Biological Interest (>2400 terms)

12. FAIR Vocabularies: Development

The IEDB has also developed the MHC Restriction Ontology, following OBO principles:

http://purl.obolibrary.org/obo/MRO

12. FAIR Vocabularies: Public

Sometimes there is no good home for a term that we need: mouse/rat strains, post-translational modifications of proteins, etc.

We put these terms in an application ontology ONTIE, then migrate to better homes when available.

ONTIE is now public with PURLs and RDF/OWL representations in multiple formats:

https://ontology.iedb.org/ontology/ONTIE_0002032

ONTIE Terms

ONTIE:0002032 Polymerase basic protein 2 (Influenza A virus)

https://ontology.iedb.org/ontology/ONTIE_0002032

- type: owl:Class
- label: Polymerase basic protein 2 (Influenza A virus)
- alternative term: PB2
- alternative term: RNA-directed RNA polymerase subunit P3
- IEDB alternative term: Polymerase basic protein 2
- · template: protein class
- · ONTIE domain: protein
- protein label: Polymerase basic protein 2
- protein taxon: Influenza A virus

Other formats: Turtle (ttl), JSON-LD (json), TSV (tsv).

12. FAIR Vocabularies: Improvements

We can do better!

We want to do a better job of explaining to users how vocabularies are used.

One example: our assays often compose a method with a GO process.

13. Metadata Link to Metadata

The IEDB links to many resources (I2), which link to other resources, which link to other resources, ...

R1.1. License

The IEDB was failing this principle.

The IEDB's content is available under the Creative Commons Attribution 4.0 International license. We are making this clear with human- and machine-readable annotations.

R1.2. Provenance

The IEDB uses PubMed IDs to link to the original article.

We are using PROV and adding metadata about our generation of the metadata from an original source.

R1.3. Community

We are careful to use standards that are appropriate for the immunology community.

Summary: Playing FAIR

- ► F3: Standardize identification of journal parts (Figures / Tables)
- ▶ F4: Add IEDB metadata to Biosharing, Biocaddie and Wikidata
- ▶ A1: Provide machine actionable representation of IEDB assay level data
- ▶ I1: Represent the IEDB data in RDF/OWL
- ▶ 12: Make all links to external vocabularies explicit
- ▶ 12: Make all internal vocabularies public via ONTIE and link to them
- ▶ R1.1: Include licensing information with the IEDB records
- ▶ R1.2: Include provenance information regarding IEDB curation



More than FAIR

FAIR is not enough.

Interoperability requires shared best practises, compatible implementations.

Full interoperability also requires shared modelling patterns – we must represent similar things in similar ways.

We see a role for OBO here, and have started coordinated modelling of immunology datasets from the IEDB, BRCs, and ImmPort.

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